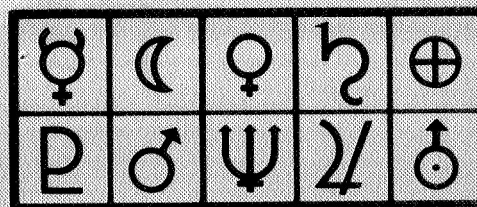


QR 9  
June 1968



PLANETARY QUARANTINE

# SANDIA LABORATORIES QUARTERLY REPORT - PLANETARY QUARANTINE PROGRAM

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Sandia Laboratories Quarterly Report - Planetary Quarantine Program

Ninth Quarterly Report of Progress  
for

Period Ending June 30, 1968

Planetary Quarantine Department  
Sandia Laboratory, Albuquerque, New Mexico

June 1968

Project Nos. 340.229.00  
340.229.01

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The following is a summary of the activities being pursued, and the progress made, during the second quarter of calendar year 1968.

1. Dry Heat Sterilization Modeling and Supportive Experimentation

- A. Description. A thorough understanding of microbial death is needed if planetary quarantine policies are to be confidently achieved. A model based on a physical understanding of sterilization of organisms should yield more confident predictions in ranges where data is unavailable.
- B. Progress. Dry heat sterilization experiments were conducted to establish basic modeling parameters. These parameters are to be utilized in model validation and in future laboratory and computer experiments with variable temperature profiles.

The technique involves seven basic steps which are performed in the laminar down-flow clean room. These steps are:

1. Bacillus spores are pipetted onto the surface of aluminum strips.
2. Water is removed by dessication for at least 16 hours.
3. Immediately after removal from the dessicator, the spores are placed into a specially modified oven operated at a predetermined temperature in the range of 125°C - 145°C.
4. After a given time lapse, the aluminum strips are removed from the oven and placed on cooled aluminum slabs.
5. The strips are then placed into 10 ml of H<sub>2</sub>O and insonated for two minutes.
6. The spores are diluted to an appropriate level and plated with trypticase soy agar in petri dishes.
7. The petri dishes are then incubated at 35°C for 48-72 hours and the resulting colonies are counted.

Graphs 1a, 1b, and 1c show the experimental survival data expressed as ratio of survivors to initial population for temperatures of 125°C, 135°C, and 145°C, respectively. The observed survivors are indicated by circles, x's, or squares. The curves represent predicted survivors from the equation

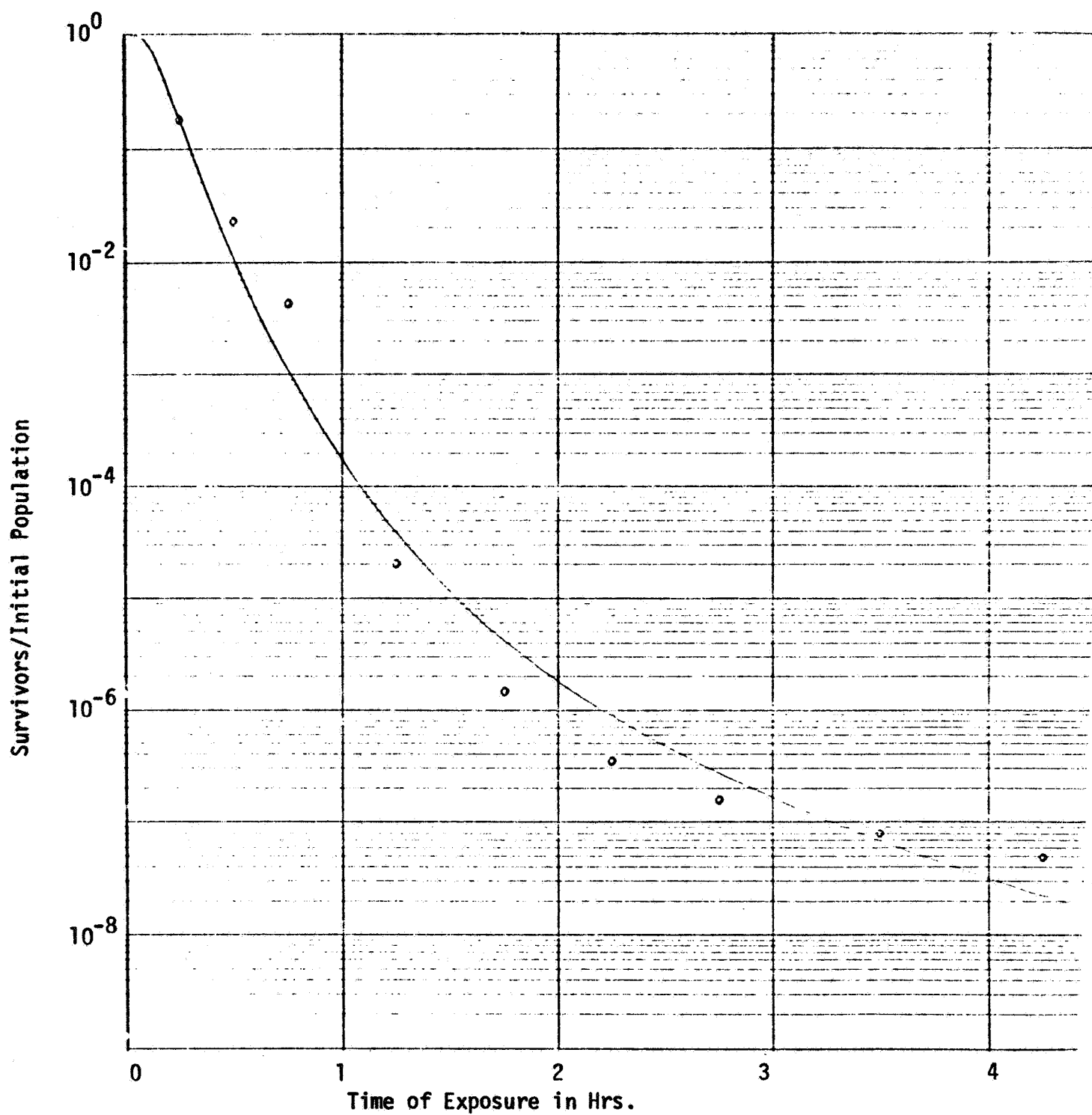
$$p(t) = \left\{ 1 - \left[ 1 - \frac{(k_1 e^{-(k_1 + k_{-1})t} + k_{-1})^2}{k_1 + k_{-1}} \right] \right\} \times \frac{1}{1 + 50k_2 t} \sum_{j=6}^{50} \binom{50}{j} (50k_2)^{50-j}$$

where, from absolute reaction rate theory,

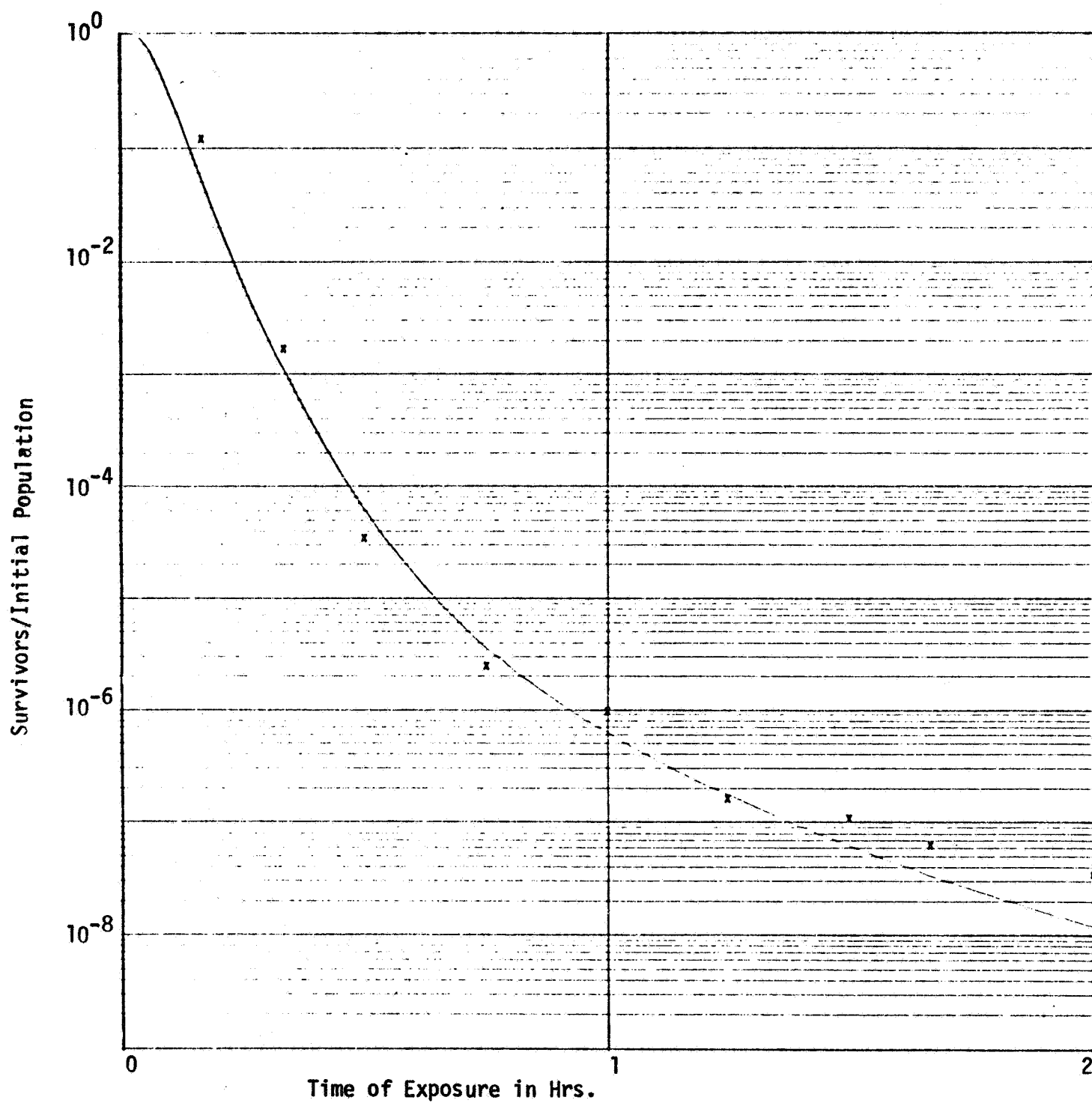
$$k_i = \frac{kT}{h} e^{-\Delta F^\ddagger / RT} \quad i = 1, 2, 3 \text{ and } \Delta F^\ddagger = \Delta H^\ddagger - T\Delta S^\ddagger.$$

In this equation  $p(t)$  represents probability of single spore survival at time  $t$  under the assumption that there are two competing sterilization mechanisms. One is a reversible first order reaction (forward rate  $k_1$ , reverse rate  $k_{-1}$ ) inactivating two molecules and the other is a second order reaction (rate  $k_2$ ) which sterilizes if fewer than six of fifty molecules are active.

Comparisons of enthalpies and entropies to laboratory values  $\phi$ X 174 DNA and R17 RNA from Ginoza, W., Hoelle, C. J., Vessey, K.B., and Carmack, C., "Mechanisms of inactivation of single stranded virus nucleic acids by heat", Nature, Vol. 203, Aug.8, 1964, pp.606-609, were made.

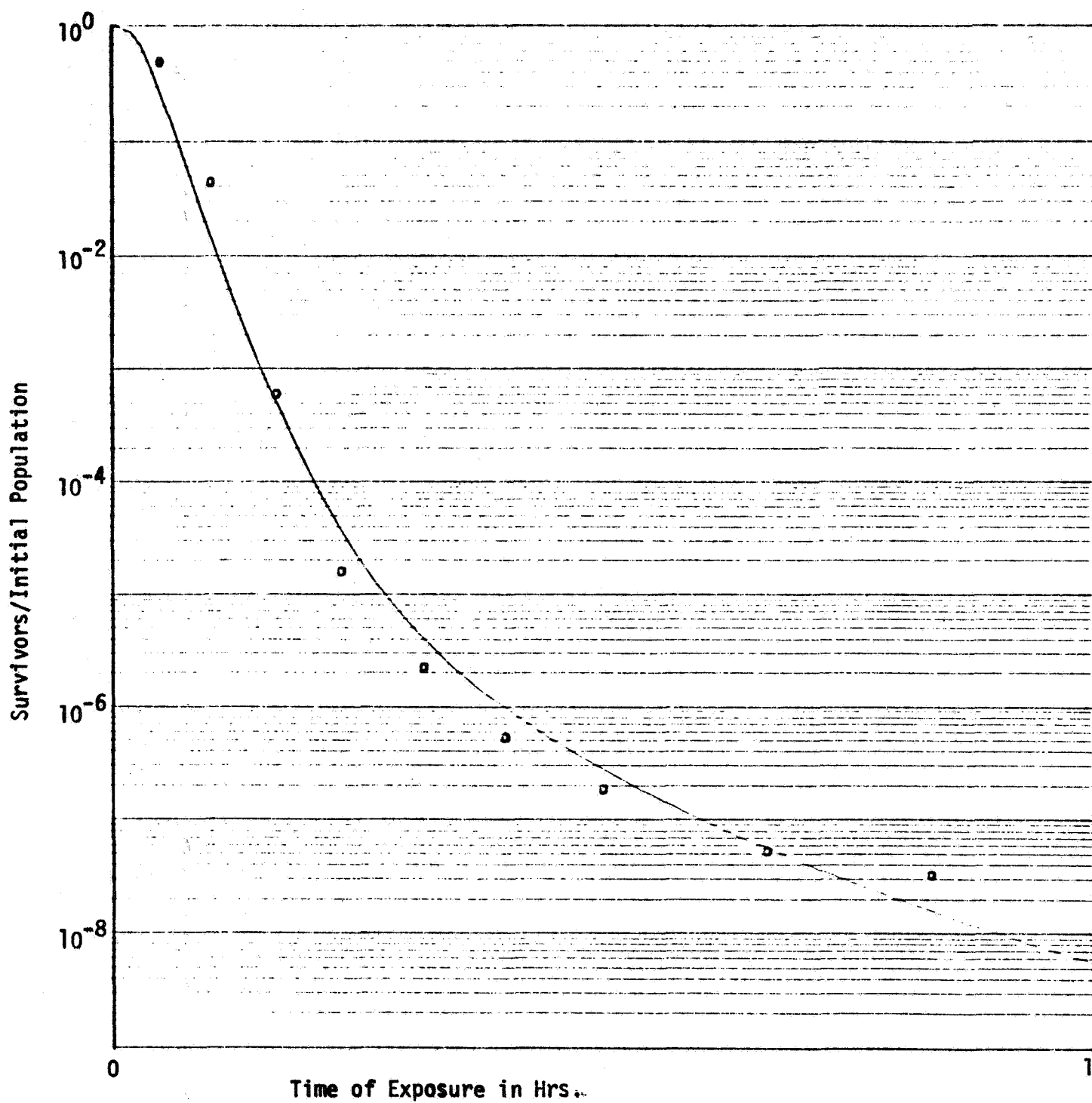


Graph 1a



Graph 1b





Graph 1c

### Experimental

$\phi$ X 174 DNA	$\Delta H^\ddagger$ k cal/mole	$\Delta S^\ddagger$ eu
pH 5.4	29.	17.
pH 6.7	35.	22.
pH 7.5	35.	21.
R17 RNA		
pH 5.4	29.	10.
pH 6.7	25.	-7.
pH 7.5	29.	5.

### From Model & Graphs 1a-1c.

$k_{-1}$	.18	-63.
$k_1$	34.4	29.1
$k_2$	21.3	-5.8

Since  $k_1$  is associated with a DNA-like first order reaction, the appropriate comparison is between experiment values and those associated with  $k_1$ .

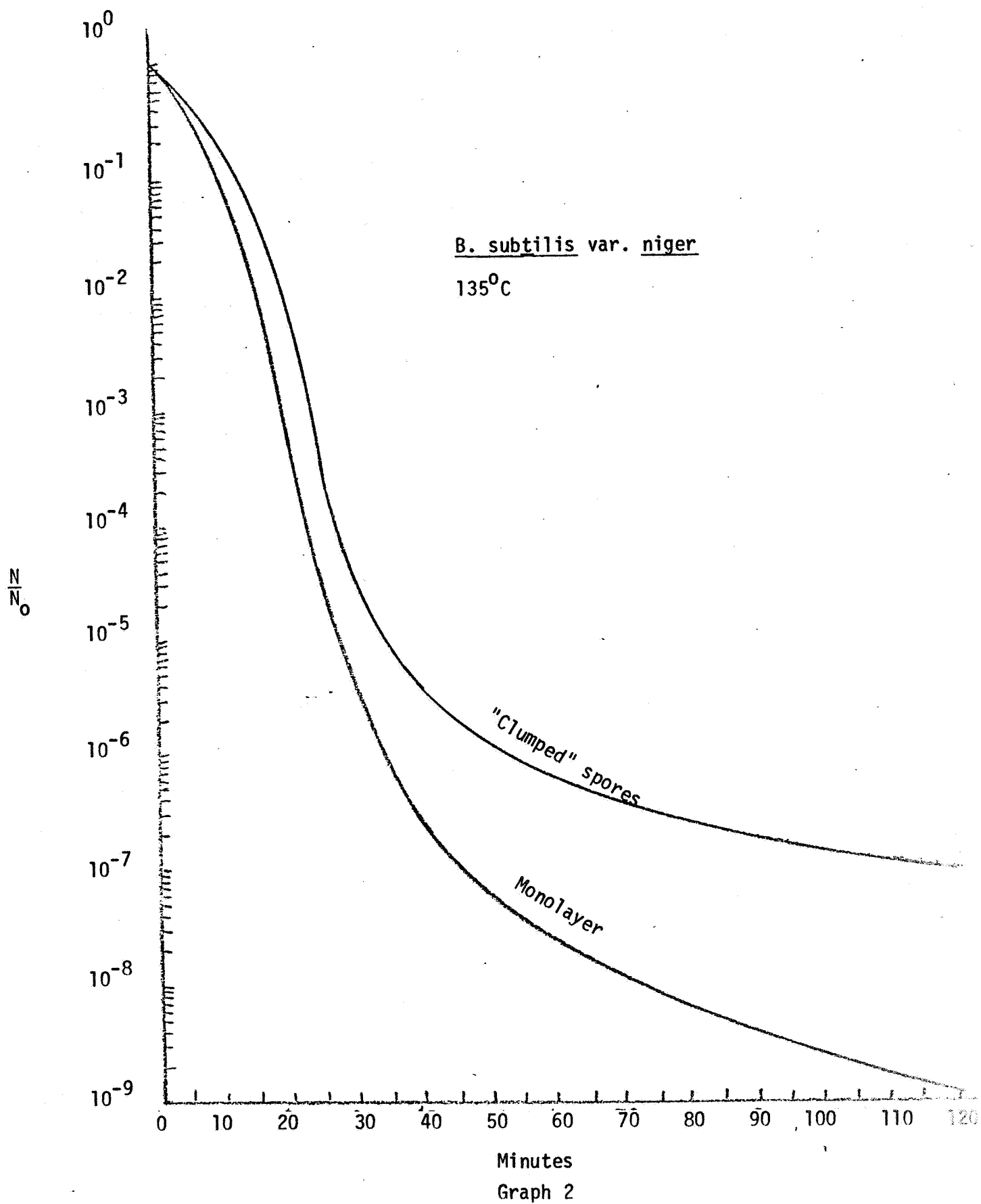
No conclusions were drawn from the comparisons but they are useful in providing intuition for future modeling experiments. For example, since double stranded DNA is expected for our test organism, could it be that we are observing a reversible denaturation of two single strands followed by a consecutive irreversible reaction?

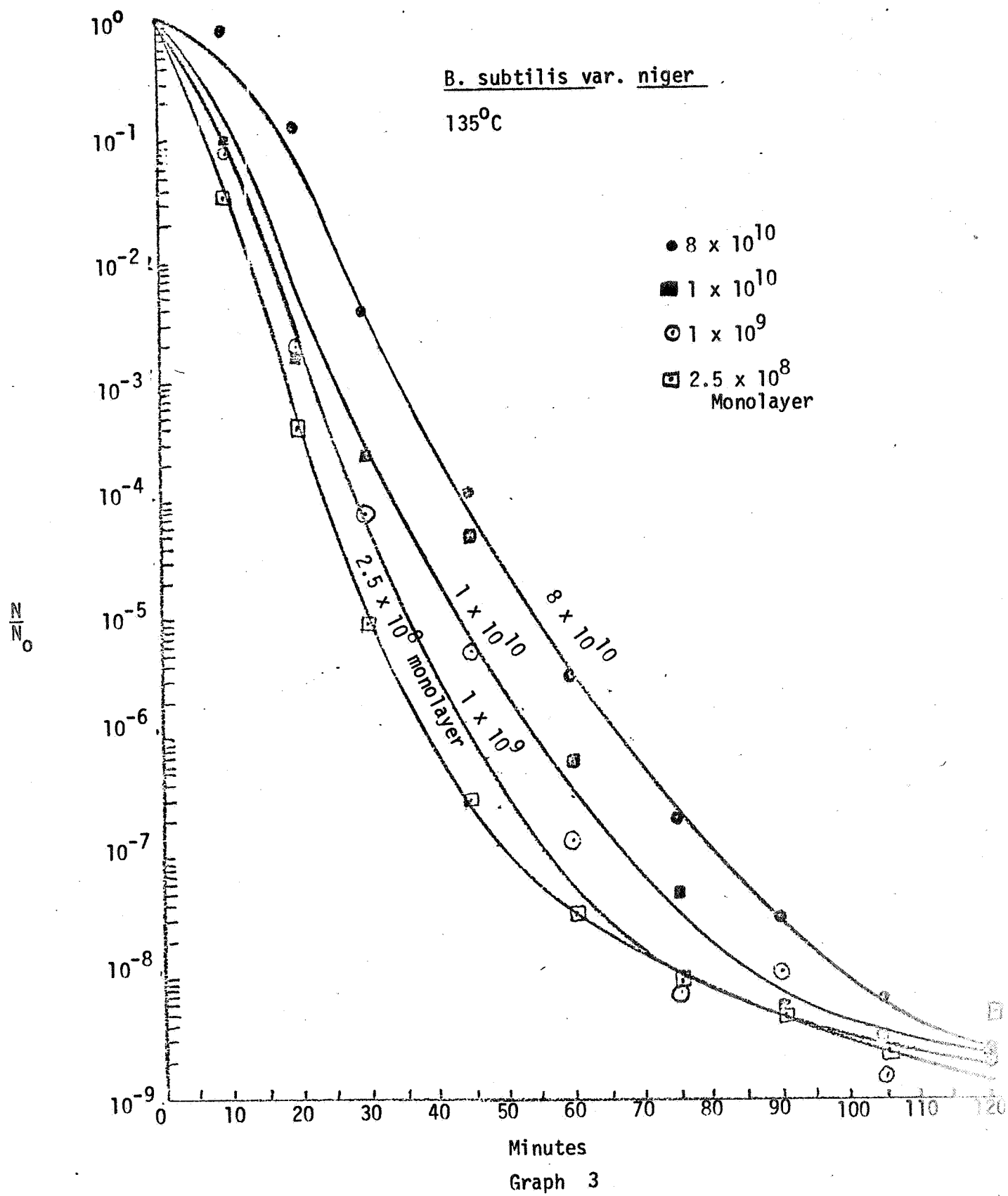
The major deviation of the data shown in Graphs 1a-1c from most death curve observations involves the tailing effect in the  $10^{-7}$ - $10^{-8}$  area of the graph. Although this effect has been noted in the open literature, an investigator could fail to observe the tail because

of a limited initial population. The tail seems to be temperature independent over the working range as evidenced by the appearance of the tail at the same survivor level for each temperature.

Microscopic observation revealed that the pipette method of spore deposition left many organisms clumped and in direct contact with each other. To determine if this had an effect on the death curve an electrostatic deposition device was constructed and a monolayer (non-clumped) of spores was deposited on the aluminum strips. Graph 2 illustrates the results of such an experiment. The two curves show the same form; however, the tail of the monolayered spores was depressed by  $1\frac{1}{2}$  - 2 log cycles indicating some protection from close packing of spores. This protection does not seem to effect the overall mechanism of spore death.

With the previously established assumption that clumping had little or no effect on the death mechanism it was decided to determine the effect of spore population or concentration on the curve. Graph 3 indicates four different concentrations of spores starting with approximately  $10^{11}$  and going down to  $2.5 \times 10^8$  spores per strip. The curves show the same amount of population drop for each concentration including the monolayered group. This would seem to contradict the previous work. Upon microscopic examination the spore suspension was seen to be heavily contaminated with residual culture medium, which was not present in the initial tests on the monolayer effect. Since the medium contained all the essential elements for spore formation it also could serve as a participant in an interchange of materials in and out of the spore. This could provide the same protective activities associated with clumped cells.



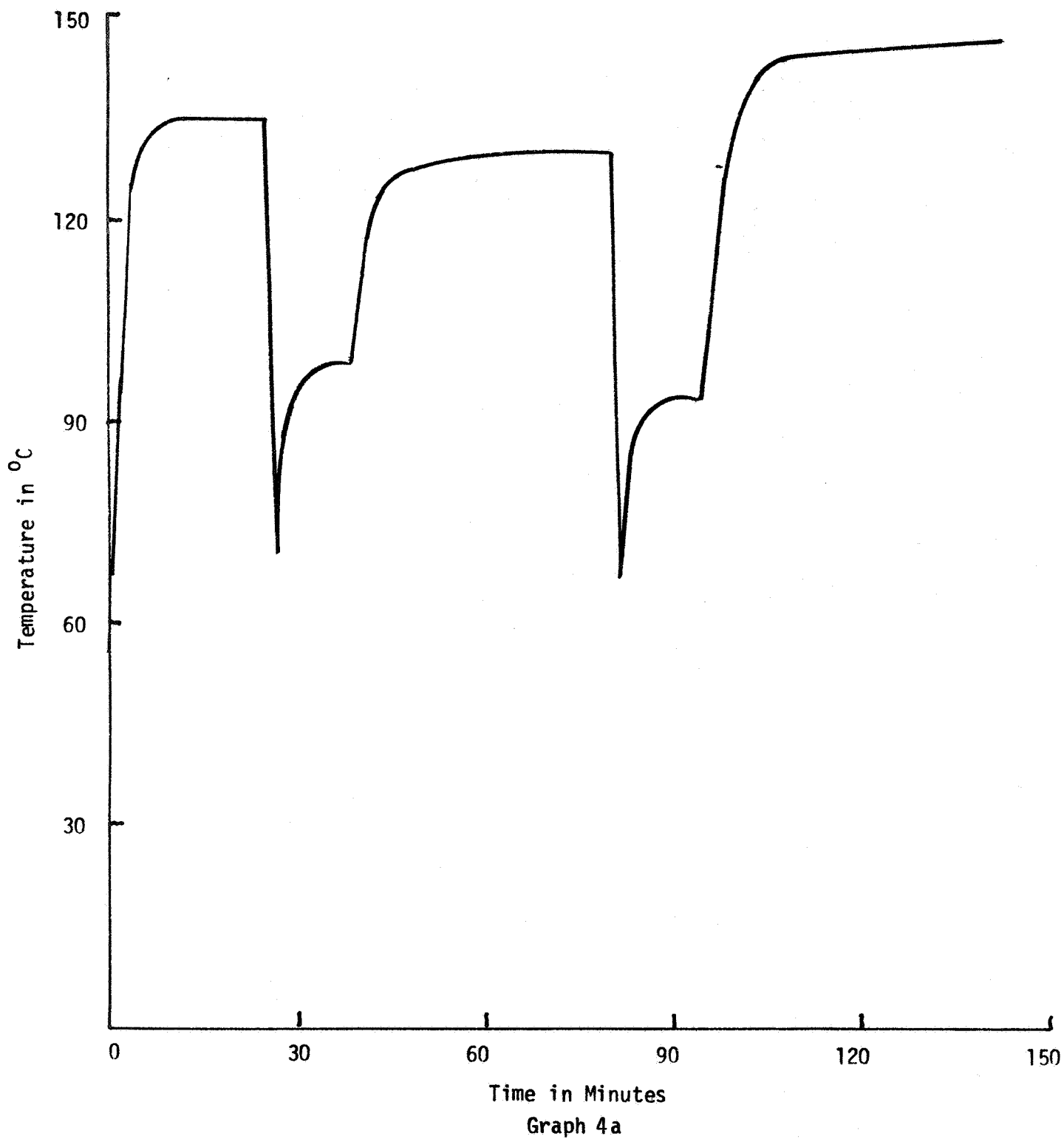


The similarity of the curves for varying concentrations has direct bearing on the extrapolation of the death curves below the probability of one survivor from any given population of spores. Results obtained below this level of probability are difficult to interpret because of the low ratio of viable organisms to total samples involved. Contamination from extraneous sources can greatly influence the ratio obtained with a resulting low level of confidence in the data.

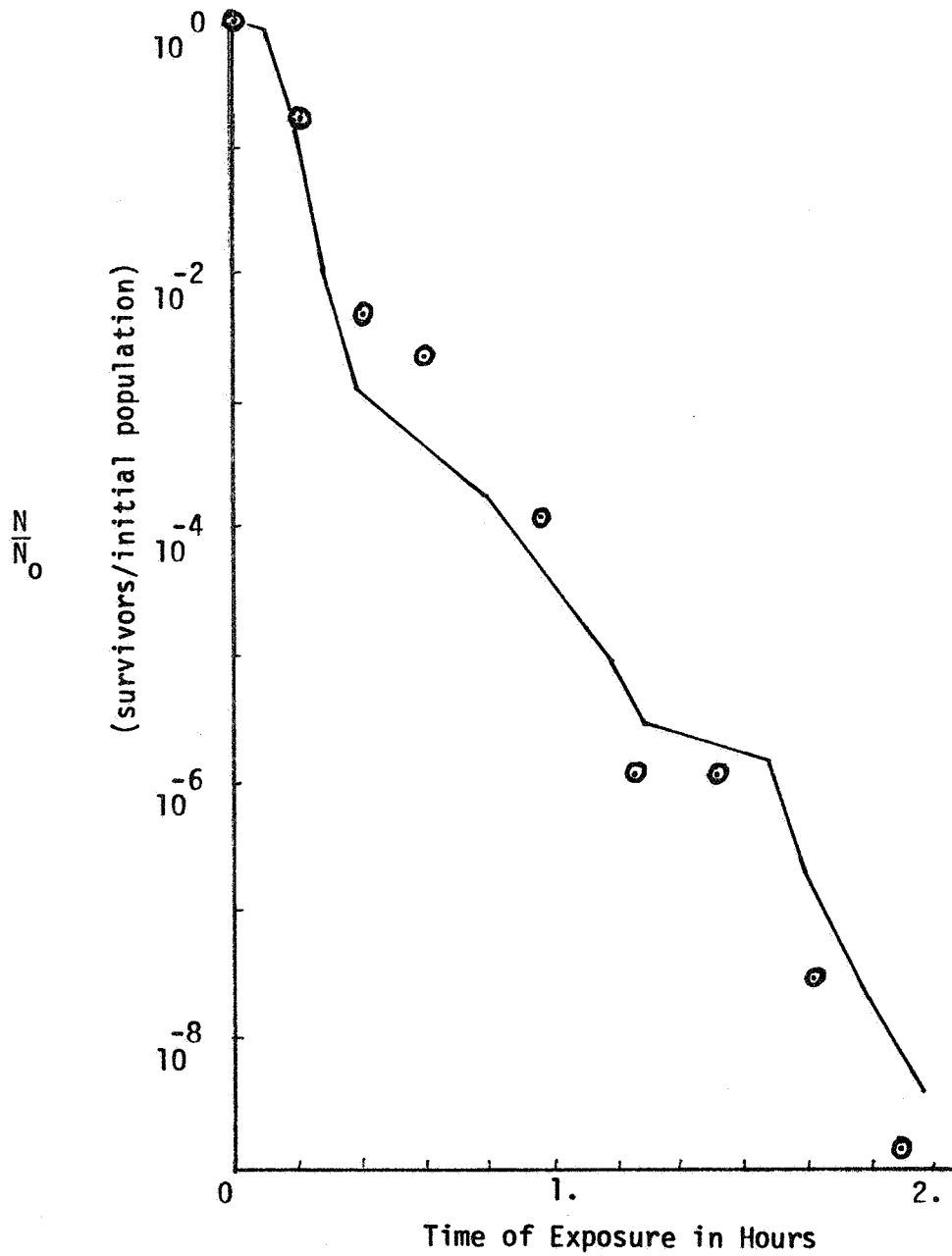
A variable temperature profile experiment was conducted in which the spores were exposed to the temperature profile shown in Graph 4a. The ratio of survivors to initial population is indicated by the circles in Graph 4b. The solid line graph in 4b is the computer run giving the predicted survivor ratio which results from incorporation of the variable temperature profile into the mathematical model. To facilitate initial computation, the Arrhenius equation was used for reaction rate determinations instead of the equation from absolute reaction rate theory. The investigation is being continued with this additional refinement.

After studying the variable temperature profile data, it was noted that there was very little evidence of a tail after a 9 log drop, even though uniform heating had produced a tailing effect after 6-7 logs.

To further study these apparent phenomena, a series of heat profiles were run and the results are shown in Graph 5. Rapid cooling of the spores showed no change in the death curve. When the spores were cooled slowly the resulting death curve duplicated that of the beginning portion of the death curve between time 10-45 minutes.

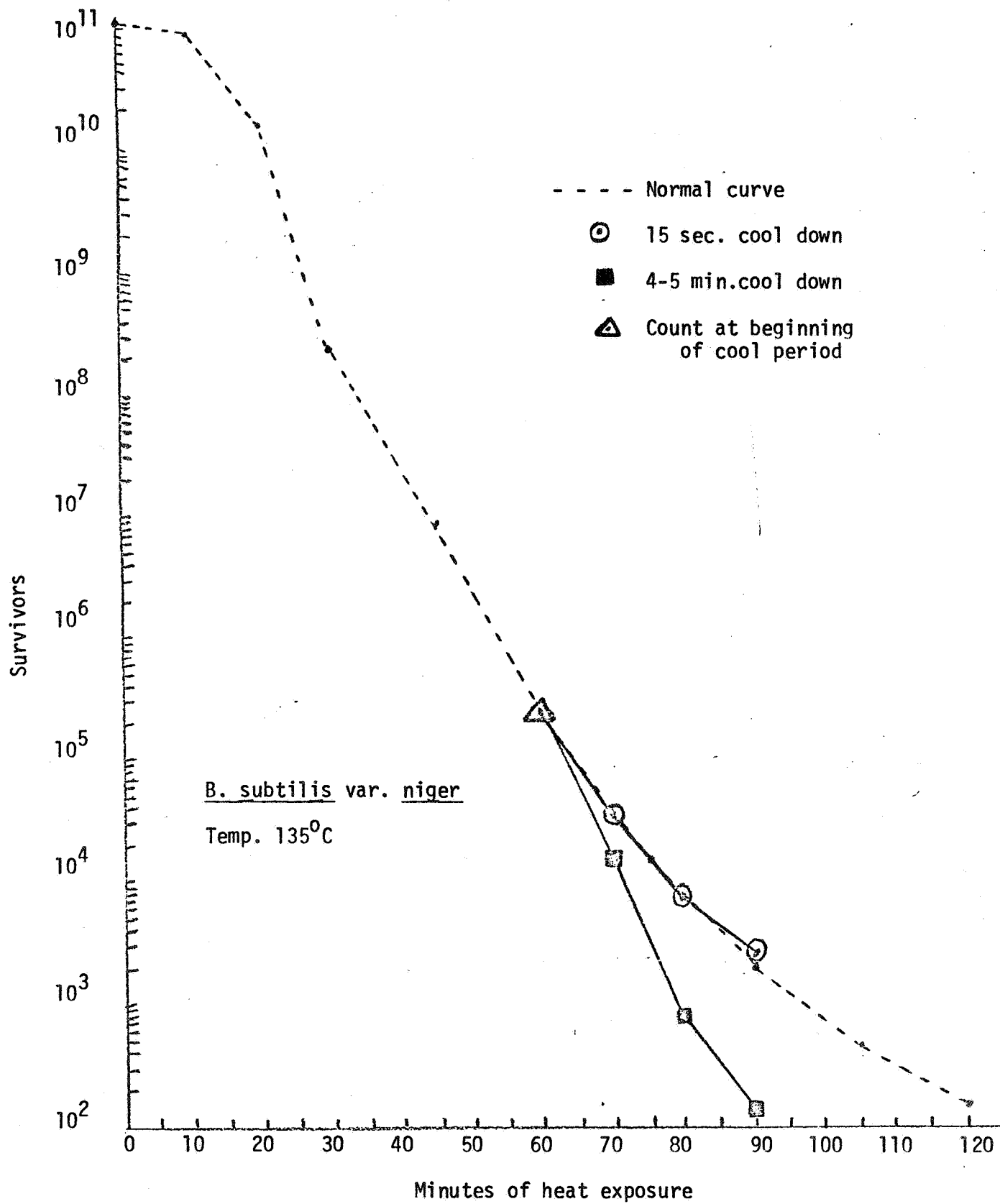


A Comparison of Experimental Results With  
Modeling Predictions With a Variable Temperature Profile



Graph 4b





Graph 5

Future studies are planned for evaluation of dry heat curve parameters and their relationship to changes in spore chemical compositions with respect to time at a given temperature.

## 2. Design of a Lunar Information System

- A. Description. The objective of this activity is to design an information system that will provide the outputs necessary for meeting planetary quarantine lunar responsibilities as defined in NASA policy.
- B. Progress. Such a design was completed this quarter. The system is comprised of four major portions: A file preparation subsystem, a data storage subsystem, a lunar inventory subsystem and a communications subsystem.

The file preparation routine design specifies the way in which

- 1) module, suit and astronaut identifications are stored,
- 2) launch dates, launch pads and landing coordinates are stored,
- 3) environmental sampling locations are stored,
- 4) environmental sampling locations are related to the building in which they are located,
- 5) directories relating
  - a) astronauts and suits to flights
  - b) modules to flights
  - c) dates and landing coordinates to flights,
  - d) environmental locations to buildings,

- e) modules to buildings, and
  - f) file locations to the above information,
- are established,
- 6) tape and disk records are sorted to update directories in case of mission changes, and
  - 7) cancelled flights are removed from active files.

In designing this subsystem, complete parameter formats, and formats for all of the above files were specified.

The data storage routine design specifies the way in which:

- 1) microbial assay data is stored (in all of its various forms),
- 2) to specify
  - a. the date on which data was acquired,
  - b. the type of data it is, and
  - c. its source (module, suit, and so forth),
- 3) to call data processing subroutines including all models associated with quantitative and qualitative bioburden estimations and predictions, and
- 4) to store the calculated results in permanent type files and a temporary disk file.

In designing this subsystem, all formats for the above files were specified.

The lunar inventory routine design specifies the way in which

- 1) all bioburden information on flights that have reached the lunar surface is to be stored,
- 2) call model subroutines to update the lunar inventory,
- 3) call subroutines to predict contamination density near specified lunar coordinates, and

- 4) call subroutines to predict the likelihood of contaminating a lunar sample.

The design of this subsystem included specification of all formats for these files.

Finally, the communication routine design provides a language for requesting outputs from the computer and a format and user guide for utilizing this language. All output formats are designed.

There are several "safety" features provided by the system design. First, since the exact approach to implementing NASA lunar planetary quarantine policy is unknown, the system design allows for sufficiently many outputs and inputs to assure a meaningful working system after detailed policy is firm. In addition, the system is modularized in the sense that all models are subroutines that may be easily changed. Thus, if certain models are found inadequate or requirements for processing change, the models may be replaced without changing the basic system design. This offers an additional advantage in that the basic system may be made operational without exact knowledge of the models. Other "safety" features include: provisions for updating flight specifications in the event that flight schedules, hardware or personnel should change; data checking and correction procedures, and a complete information retrieval scheme allowing any information or data previously stored to be retrieved at any time.

The design of the system includes detailed flow charts of each of the four subsystems described above with an accompanying description for the rationale of each set of flow charts. A document entitled,

"An Interactive Information Computer System for Planetary Quarantine for Lunar Programs" by A. L. Roark and A. L. Wyer is nearing publication.

3. Lunar Inventory Model for Automated Missions

- A. Description. The objective of this activity was the development of a model, and associated code for use in the information system described in 2. above, to (i) estimate the lunar density of terrestrial organisms deposited by automated missions as a function of lunar coordinates and time and (ii) estimate the probability that a lunar sample will contain one or more terrestrial organisms deposited by automated missions, again, as a function of location and time.
- B. Progress. Such a study for automated missions was completed this quarter. The study consists of five parts: Initial burdens, burden change in cislunar space, dissemination mechanisms at the lunar surface, bioburden changes on the lunar surface and probability of sample contamination.

Estimates of initial (at launch) burdens of automated lunar capsules provided by NASA as a result of a sampling program were compared with expected burdens based upon general environmental data. A quantitative surface burden model (briefly described in Quarterly Report QR 8) was used in making this comparison. On this comparative basis, all data provided by NASA Headquarters appeared to be conservative in the sense that predicted burdens did not exceed NASA estimates. The NASA estimates were subsequently used. In addition, based on the model, one would not expect great deviations from these estimates.

Based on spacecraft and environmental data the initial burdens were decomposed into "categories", including sporeforming organisms, vegetative organisms, exposed organisms and occluded and embedded organisms.

The effects of various physical phenomena in cislunar space on each category of organism was assessed. Among the phenomena considered were: space capsule temperatures, vacuum, solar ultra-violet radiation, solar ionizing radiation, magnetosphere protection and "near-earth" radiation belts. The general conclusion reached was that, in no case, did the burden at impact exceed 30% of the burden at launch.

Two possible means of distributing a lunar probe's bioburden about the lunar surface were used: transport in crater ejecta and transport on space probe fragments. Other types of transport mechanisms were considered and generally discounted as being unimportant or yielding results somewhere between the "extremes" provided by the two mechanisms used.

In examining the transport mode when all microorganisms are attached to parts of the spacecraft, the assumption was that spacecraft break-up is explosive at the known hard impact velocities. This situation was analyzed to provide both particle velocity and particle range spectrums. Assuming a uniform spatial bioburden, a lunar bioburden density was then obtained.

In the case where it was assumed that all microorganisms were contained in crater debris, calculations were based upon the work of Gault, Shoemaker and Moore ("Spray Ejected from the Lunar Surface by Meteoroid Impact", NASA-TN-D-1767, April, 1963). First,

the mass of soil excavated was determined as a function of impact energy. The dispersal of this mass was then analyzed, and the result were graphs of organism density on the lunar surface as a function of distance from impact site. Finally, the long term time dependence of this burden was analysed.

For each of the two dispersal mechanisms, the probability of sample contamination was calculated per square centimeter of surface taken.

The conclusions drawn were of a "conservative" nature. These were:

1. Fewer than 30% of the microorganisms residing on a typical U.S. lunar probe at launch time survive transit to the moon. The thermal kill of organisms during the typical 34-80 hour transit times can be neglected.
2. Seven or eight months after touch-down, the contaminated area around the landing point of a typical U.S. unmanned probe that has made a soft landing should be confined within a conservative radius of 100 meters.
3. Organisms remaining on fragments of a typical U.S. lunar probe that has made a hard impact on the moon should be confined almost entirely within a conservative radius of 50-60 kilometers about the impact point. These may remain viable for indefinite periods of time.
4. Organisms carried by the crater material formed in the hard impact of a typical U.S. lunar probe may be deposited over the entire surface of the moon. Seven to eight months after impact, however, the contamination of the lunar surface from this dispersal mechanism should be negligible.

5. The distance from the site of hard impact of a typical U.S. lunar probe at which the assumption of uniform deposition of the probe's bioburden over the entire lunar surface becomes a conservative assumption is 240-260 kilometers.

A report, "The Chances of Retrieval of Viable Microorganisms Deposited on the Moon by Unmanned Lunar Probes" by M.S.Tierney, is being prepared for printing.

4. A Model for the Optimal Identification of Bacteria

- A. Description. There are two subroutines dealing with qualitative bioburden estimation and prediction needed in the aforementioned information system. First, a model to assess the likelihood that all types of organisms of concern that are present have, indeed, been identified. Results of this form depend on the number of samples taken and the results of those samples. Second, the system requires a means of determining the smallest number of tests needed to identify an unknown microorganism, given that it is known to belong to a "class" of organisms about which concern exists. Based on this smallest number of tests, a computer identification subroutine is needed.
- B. Progress. Some progress has been made in the first area mentioned above. It is now known that the minimum number of samples,  $M$ , to identify all types,  $N$ , of organisms of concern with a given probability cannot be determined a priori when  $N$  is unknown. There is a strong dependence of  $M$  on  $N$ , and this is being investigated.

A model to provide a "best test set" was completed this quarter. The model requires theoretical inputs of the form shown in the accompanying table.



	test 1	test 2....test j....test n
organism 1	0	1 .... 0 .... 1
organism 2	1	0 .... 0 .... 0
⋮	⋮	⋮
organism i	0	G .... 1 .... 0
⋮	⋮	⋮
organism m	G	1 .... 0 .... G

The set of organisms 1 through m is that collection of **organisms** for whose existence concern has been expressed. The collection of tests 1 through n is the set of all tests one is willing to use in order to determine which of the listed organisms a given unknown organism is. If the list is "properly" defined, a few additional tests will determine whether an unknown organism is or is not one of those listed. The concern of the model is which organism it is. Entries in the table above represent known results of applying test j to organism i ( $j = 1, \dots, n; i = 1, \dots, m$ ). As illustrated, these are 0 (negative result) 1 (positive result) or G (a number larger than 1 representing that the information is unknown). The model will accept any test results that are discretized, that is, they need not be only zeros and one's as in the illustration. Data may be specified at any given confidence level in the sense of Rypka, et.al. ("A Model for the Identification of Bacteria", J.Gen.Microbiol. 46 (1967).

An organism in the list, say organism 1, may be identified by the tests 1 through n, if for each other organism, there is at least one test which gives a different physical outcome when applied to organism 1 and the other organism. Thus, organism identification

relates to the ability of the given tests to physically distinguish between (or separate) pairs of distinct organisms. There are  $m(m-1)/2$  possible pairs of distinct organisms. Any collection of tests, say  $T = \{\text{test 1, test 2, ..., test n}\}$  will separate  $K_T$  of these pairs. It is entirely possible that some proper subset  $T'$  of  $T$  will separate exactly the same number of pairs, i.e.,  $K_T = K_{T'}$ . When this occurs,  $T'$  will, perforce, separate the same pairs. Thus, such a subset  $T'$  of  $T$  has exactly the same identification ability as the original test set  $T$ .

The identification model determines a subset  $T'$  of  $T$  with the properties (i)  $T'$  has exactly the same identification ability as the original set  $T$  of tests and (ii) this statement cannot be made of any smaller subset of  $T$  than  $T'$ . In this sense, the model determines a "smallest" test set which will identify the given organisms as well as the original test set.

To do this, the original data is used to form a pair separation table. As in the previous table, the columns correspond to tests. Here, however, the rows correspond to pairs of organisms. This is illustrated in the accompanying table.

	test 1	test 2	...	test n
(org.1,org.2)	0	1	...	0
(org.1,org.3)	1	1	...	1
⋮	⋮	⋮		⋮
(org.i,org.j)	0	0	...	0
⋮	⋮	⋮		⋮
(org.m-1,org.m)	1	0	...	1

The entry in the  $i$ th row and  $j$ th column of pair separation table is 1 if the pair associated with the  $i$ th row is separated by the  $j$ th test and 0 otherwise. Pairs corresponding to rows containing only zero entries, cannot be separated by the given tests. Such rows are discarded, and the remaining rows form a reduced pair separation table. The entries of this new table are denoted  $a_{ij}$ , and they are always zero or one. No row contains all zeros.

A (0,1) linear programming problem of the form

$$\text{minimize } \sum_{j=1}^n x_j$$

so that, for each row,  $i$ , of the reduced pair separation table

$$\sum_{j=1}^n a_{ij}x_j \geq 1 \quad (\text{all } i)$$

and  $x_j$  is 0 or 1, is formulated. This, in effect, constitutes the "best test set" model.

A solution of the above (0,1) linear programming problem is interpreted in the following way. Let

$T'$  be the set of tests  
corresponding to  $x_j$ 's that  
are 1.

Thus, if  $x_1 = 1$  in the solution, test 1 is included in  $T'$ .

The set  $T'$  constructed in this way has the properties (i) that  $T'$  has exactly the same identification ability as the original test set, and (ii) no subset of the original test set smaller than  $T'$  has the same identification ability as the original test set. That is, the test set  $T'$  so defined is a "best test set".

A computer code has been prepared, and several problems provided by the Public Health Service and some problems taken from the literature have been successfully solved. A computerized identification scheme is being programmed. A detailed report of this work is being prepared.

5. Fine Particle Studies

A. Description. Experimentation conducted during this quarter was oriented toward behavior of particles on surfaces. In order to conduct such studies realistically, particles should be used to simulate actual contamination expected during spacecraft assembly conditions. This laboratory, and others, have studied natural occurring particles for behavior on surfaces with limited success. Most of such studies have been based on bacterial content of particles for indicators; however, several problems with ambient particles make such studies very difficult. The main problems are low bacteria content on particles found in normal environments and the difficulty of obtaining control or reference bacterial levels. Experimentation has been directed toward developing test particles, techniques for their dissemination, and techniques for their detection.

B. Progress. The following techniques for producing, disseminating, and detecting particles are now being studied.

1. Particle Tagging. Two techniques, described in the last quarterly report, to tag particles with viable spores have been examined more thoroughly.

a. Mechanical Mixing of Spores and Inert Particles. A method described by Norman L. Peterson of CDC USPHS in Phoenix has been tested. By this method approximately  $1 \times 10^{11}$

Bacillus subtilis var. niger spores were mixed with several grams of 10  $\mu$  aluminum oxide particles. The mixture was dried in a vacuum oven at 40°C. The dried mixture was aerosolized by blasting a few seconds with an air jet. The tagged particles were settled out on petri dishes filled with nutrient agar; the plates were incubated overnight. By counting the colonies microscopically and examining whether the colonies had particles in the center, a percentage tag was determined. Fewer than 1% of the colonies were caused by free spores. Ninety percent of the 10  $\mu$  particles were tagged.

- b. Electrostatic Tagging of Particles. The electrostatic tagging instrument was used with sifted vacuum cleaner dust and Bacillus subtilis var. niger spores. Several tests were run. By varying the air velocity used to separate the spores from the larger particles, various particle sizes could be selected. When > 30  $\mu$  particles were selected a 20% tag was achieved. When > 50  $\mu$  particles were selected a 50% tag was achieved.

2. Acoustic Particle Disseminator. The only device available at Sandia to supply a continuous output of dry particles is a Wright dust feeder. The disadvantage of this machine is that it crushes a high percentage of the particles used. This condition obscured the results desired in several experiments. A first model of a new instrument to disseminate dust has been constructed and tested, and a working model is under construction. The new disseminator keeps the dust in a liquid-like state

(fluidized bed) by agitating it in a speaker cone. Air is passed from below to drive the particles suspended in the air from the chamber. These particles are driven into a plate impactor to separate any agglomerates. The output of the first device constructed - minus the impactor - was fed to a photometer. The output was constant within 10% over a 20 minute period. The first device would not hold enough pressure to drive the impactor, but the working model will hold the higher pressure necessary.

3. Vacuum Probes. Fifty of the newest vacuum probes have been constructed. Twenty-four were sent to Normal L. Peterson of CDC USPHS in Phoenix for evaluation, and one was sent to Larry Hall of NASA in Washington, D. C., for demonstration. The remainder of the probes are to be used for surface-particle studies at Sandia.

6. Electrostatic Deposition Device

- A. Description. The results listed in Section 1 above from the dry heat inactivation studies currently being conducted will be used as a basis for predicting the exposure time needed for bacterial spore inactivation. To more nearly duplicate the actual distribution of bacterial contamination found on spacecraft, a piece of equipment was constructed for the production of a monolayer of bacterial spores. This was necessary because the usual method of deposition (pipetting) caused some clumping or aggregation of the bacterial spores. It has been postulated that this clumping does have some effect on the inactivation of microorganisms.

B. Progress. The electrostatic deposition device consists of a 15 inch, 3 RPM, plastic turntable with a concentric metal strip placed one inch from the outer edge. This strip provides the electrical contact for the aluminum sample strip. Two nebulizers provide the bacterial aerosol and are directed tangential to the edge of the turntable. The bacterial spores are deposited by applying a 12 KV negative potential at the orifice of the nebulizers and a 20 KV positive potential at the turntable. The turntable is rotated during the period of aerosol production by the nebulizers.

The layer of spores deposited is uniform with a maximum variation between one inch square strips of 20% with a loading of approximately  $10^8$  organisms per strip. This variation is similar to that found for the pipette method of deposition. After a certain loading density the number of bacterial spores deposited on a strip appears to show little dependence on the spore concentration in the nebulizers. The maximum loading of the sample strips with spores seems to occur near the level of  $10^8$  spores per square inch. When using  $2 \times 10^{11}$  total spores in the nebulizer a resulting deposition of  $1 - 3 \times 10^8$  spores per strip was found, whereas, a  $10^{10}$  spore loading in the nebulizer deposited a layer ranging from  $0.5 - 2 \times 10^8$  spores per strip. In all cases when viewed under a microscope the spores appeared as discrete structures with a minimum amount of contact between the spores.

7. Contamination Control Study (NASA Contract No. H-13245A)

A. Description. This project involves preparation of the NASA Contamination Control Handbook. This document is a "first" of its kind and the only technically-oriented handbook that encompasses all aspects

of the subject. Technical information and data, representing many technical disciplines, are provided for persons engaged in the field of contamination control.

A preliminary copy of the NASA Handbook has been published as Sandia Laboratories Report No. SC-M-68-370. It consists of 366 pages with 95 tables and 57 figures in 12 sections as listed below.

Section

- 1 Introduction to Contamination Control
- 2 Contamination Control in Product Design
- 3 Control of Surface Contamination
- 4 Contamination Control in Gases and Liquids
- 5 Control of Airborne Contamination
- 6 Microbial Contamination and Its Control
- 7 Radiation
- 8 Packaging
- 9 Handling and Storage
- 10 Personnel
- 11 Glossary
- 12 Acknowledgments

Each section contains fundamental information on the subjects covered along with detailed technical information applicable to specific contamination control situations. Sectional bibliographies are also provided for additional study.

- B. Progress. Levels of accomplishment during the quarter are shown by the following activities:
1. Approximately 80 pages of new handbook material were prepared in rough draft form. This material includes technical information



tables, charts and sketches on the following subjects:

- a. Removal of contaminants from liquids
  - b. Monitoring of nonlaminar and laminar air-flow facilities
  - c. Testing of filters and filter banks
  - d. Specifications for laminar air-flow clean rooms
  - e. Radiation as a contaminant and its control
2. Bibliographies were completed for the remaining three sections requiring them.
  3. A glossary of terms used in the handbook was prepared.
  4. A list of companies and agencies that contributed data, information or assistance in the preparation of the handbook was prepared.
  5. All material was reviewed with the technical editorial staff for layout and preparation in final form.
  6. All material was prepared in final form on reproducible masters by the Technical Information Division.
  7. The reproducible masters were proofed and reviewed for technical and editorial correctness, with corrections and revisions incorporated for final publication.
  8. Printing of the handbook was completed under the supervision of the Technical Information Division
  9. Preliminary copies of the NASA Contamination Control Handbook were distributed to NASA centers for review, pending final publication by NASA.

8. Publications

- a. J. P. Brannen, "A Rational Model for Thermal Sterilization of Microorganisms", Mathematical Biosciences, Vol. 2, Nos 1-2, (1968).

- b. C. A. Trauth, Jr., "A Multi-stage Decision Model for Mission Non-Contamination Requirements", Space Life Sciences, Vol. 1, No. 1, (1968).
  - c. J. P. Brannen, "On Logarithmic Extrapolation of Microbial Survivor Curves for Planetary Quarantine Requirements", Space Life Sciences, Vol. 1, No. 1 (1968).
  - d. D. M. Garst, K. F. Lindell, and W. J. Whitfield, "Contamination Control Handbook," SC-M-68-370, has been submitted to the George C. Marshall Space Flight Center, Huntsville, Alabama, in accordance with NASA Order No. H-13245A, for review by NASA personnel.
9. Presentations
- a. A. L. Roark, "Description of Sandia Planetary Quarantine Systems Studies Activities", First Spacecraft Sterilization Symposium, June 1968.
  - b. H. D. Sivinski, "Progress Report on Contamination Control Handbook", First Spacecraft Sterilization Symposium, June 1968.
10. Related Activities.
- a. Messrs. W. J. Whitfield, D. M. Garst, and K. F. Lindell attended the seventh annual technical meeting of the American Association for Contamination Control in Chicago, Illinois, May 13-15, 1968. Technical sessions of the meeting and visits with the exhibitors provided material and information for the handbook.
  - b. Messrs. H. D. Sivinski and W. J. Whitfield attended the NASA contract review meeting at Cape Kennedy, Florida, June 10-12, 1968. A review of the status of the handbook was presented at this meeting.

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University of Minnesota  
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Mayo Clinic  
Rochester, Minnesota 55902

Samuel Schalkowsky  
Exotech Incorporated  
525 School Street, S.W.  
Washington, D. C. 20024

Charles Craven  
Jet Propulsion Laboratory  
4800 Oak Grove Dr.  
Pasadena, California 91103

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Research Engineer  
Naval Biological Laboratory  
Naval Supply Center  
University of California, Berkeley  
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Richard G. Cornell  
Associate Professor of Statistics  
Department of Statistics  
Florida State University  
Tallahassee, Florida

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Department of Health, Ed. and Welfare  
CDC-Phoenix Field Station  
4402 North 7th Street  
Phoenix, Arizona 85014

F. N. LeDoux  
Head, Structural & Mechanical Applications Section  
Goddard Space Flight Center  
Greenbelt, Maryland

Q. Ussery  
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GSFC Sterilization Laboratory  
Goddard Space Flight Center  
Greenbelt, Maryland 20771

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Space Biology Branch  
Code 624, Bldg. 21, Rm. 161  
Goddard Space Flight Center  
Greenbelt, Maryland 20771

Robert Angelotti  
Deputy Chief, Milk and Food Research  
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Center  
Cincinnati, Ohio

Erwin Fried  
Rm.M-2101  
General Electric Company  
P. O. Box 8555  
Philadelphia, Pennsylvania 19101

Martin G. Koesterer, Microbiologist  
Bioscience Operation  
General Electric  
P. O. Box 8555  
Philadelphia, Pennsylvania 19101

Carl Bruch  
Chief, Bacteriology Branch  
Division of Microbiology  
Food and Drug Administration  
3rd & C., SW, Room 3876  
Washington, D. C. 20204

John W. Beakley  
Department of Biology  
University of New Mexico  
Albuquerque, New Mexico

Loren D. Potter, Chairman  
Department of Biology  
University of New Mexico  
Albuquerque, New Mexico

Loris W. Hughes  
Department of Biology  
University of New Mexico  
Albuquerque, New Mexico

Joe Stern  
Jet Propulsion Laboratory  
4800 Oak Grove Dr.  
Pasadena, California 91103

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